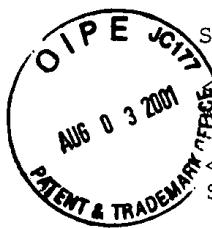


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S. Karberg, P.



**SEQUENCE LISTING**

110 > Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.,  
pong, Y. used in Tocopherol

~~Chung, Y.~~  
~~Chung, Y.~~ Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthesis

<130> 16515.054

<140> US 09/688,069  
<141> 2000-10-14

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<160> 114

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<211> 1182

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<212> PRT

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 100 105 110  
 Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr  
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 Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Val Glu Lys Val Ser  
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 180 185 190 195  
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 Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp  
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 225 230 235 240  
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 Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile  
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 325 330 335  
 Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu  
 340 345 350  
 Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys  
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gatactattt	atgcacatca	ggacaaagaa	gatgtatgaa	aagttggtgt	taagtcaaca	960
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gcccgtcat	caggacagtt	aggatggcaa	atagggacag	ctgacttattc	atctgggtct	1140
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<213> *Arabidopsis* sp.

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 35 40 45  
 Thr Lys Cys Tyr Pro Ser Trp Asn Asp Asn Tyr Gln Val Trp Ser Lys  
 50 55 60  
 Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr  
 65 70 75 80  
 Arg Leu Ile Cys Gly Met Ser Ser Ser Val Leu Glu Gly Lys  
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130	135	140
Pro Cys Met Trp Ser Ile Ala Leu Ala	Asp Pro Gly Ser Leu	Pro
145	150	155
Ser Phe Lys Tyr Met Ala Leu Phe Gly	Cys Gly Ala Leu Leu	Leu Arg
165	170	175
Gly Ala Gly Cys Thr Ile Asn Asp	Leu Leu Asp Gln Asp	Ile Asp Thr
180	185	190
Lys Val Asp Arg Thr Lys Leu Arg	Pro Ile Ala Ser	Gly Leu Leu Thr
195	200	205
Pro Phe Gln Gly Ile Gly Phe Leu Gly	Leu Gln Leu Leu	Gly Leu
210	215	220
Gly Ile Leu Leu Gln Leu Asn Asn Tyr	Ser Arg Val Leu	Gly Ala Ser
225	230	235
Ser Leu Leu Leu Val Phe Ser Tyr	Pro Leu Met Lys Arg	Phe Thr Phe
245	250	255
Trp Pro Gln Ala Phe Leu Gly	Leu Thr Ile Asn Trp	Gly Ala Leu Leu
260	265	270
Gly Trp Thr Ala Val Lys Gly	Ser Ile Ala Pro Ser	Ile Val Leu Pro
275	280	285
Leu Tyr Leu Ser Gly Val Cys	Trp Thr Leu Val	Tyr Asp Thr Ile Tyr
290	295	300
Ala His Gln Asp Lys Glu Asp Asp	Val Lys Val Gly Val	Lys Ser Thr
305	310	315
Ala Leu Arg Phe Gly Asp Asn Thr	Lys Leu Trp Leu Thr	Gly Phe Gly
325	330	335
Thr Ala Ser Ile Gly Phe Leu Ala	Leu Ser Gly Phe Ser	Ala Asp Leu
340	345	350
Gly Trp Gln Tyr Tyr Ala Ser	Leu Ala Ala Ala Ser	Gly Gln Leu Gly
355	360	365
Trp Gln Ile Gly Thr Ala Asp Leu Ser	Ser Gly Ala Asp Cys Ser	Arg
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<211> 1296

<212> DNA

<213> *Arabidopsis* sp.

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aatcgagtt	ttgccactgc	tactgcccgc	gctacagcta	cagctaccac	cggtgagatt	240
tcgtctagag	ttgcggctt	ggctggattta	gggcataact	acgctcggtt	ttattggag	300
ctttctaaag	ctaaacttag	tatgtttgt	gttgcactt	ctggaaactgg	gtatattctg	360
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gcagctggag	gttacaagat	gttgcactc	tttgatccgt	cagggaagag	aatagcagca	900
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65 Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg  
85 90 95  
Ser Ser Arg Val Val Val Ala

Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala  
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Phe Pro Gly Leu Cys Tyr Thr Cys Ala Gly Thr Met Met Ile Ala Ala  
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 Ser Ala Asn Ser Leu Asn Gln Ile Phe Glu Ile Ser Asn Asp Ser Lys  
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 165 170 175  
 Pro His Ala Val Ala Trp Ala Thr Ile Ala Gly Ala Ser Gly Ala Cys  
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 Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu  
 225 230 235 240  
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 245 250 255  
 Leu Pro Ala Ala Leu Tyr Phe Trp Gln Ile Pro His Phe Met Ala Leu  
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 Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu  
 275 280 285  
 Ser Leu Phe Asp Pro Ser Gly Lys Arg Ile Ala Ala Val Ala Leu Arg  
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 Leu Thr Ser Ser Trp Phe Cys Leu Glu Ser Thr Leu Leu Thr Leu Ala  
 325 330 335  
 Ile Ala Ala Thr Ala Phe Ser Phe Tyr Arg Asp Arg Thr Met His Lys  
 340 345 350  
 Ala Arg Lys Met Phe His Ala Ser Leu Leu Phe Leu Pro Val Phe Met  
 355 360 365  
 Ser Gly Leu Leu Leu His Arg Val Ser Asn Asp Asn Gln Gln Leu  
 370 375 380  
 Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr  
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 Gln Arg Arg Lys Lys Arg Val Ala Gln Pro Pro Val Ala Tyr Ala Ser  
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cgtatgcgtt taaccggtat ctcgacaggc attttgacgc gaagaacccg cgtactgcca	360
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catttcagg ctaaaagact tttagccgc ctgtattccg gtgtgcctca tcattaaaga	240
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<211> 297

<212> PRT

<213> Arabidopsis sp.

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20	30

25	
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35	
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70	
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70	80
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70	80
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Arg Tyr Ser Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala		
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Thr Ala Glu Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly		
165	170	175
Leu Ala Phe Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser		
180	185	190
Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile		
195	200	205
Thr Ala Pro Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu		
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Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu		
225	230	235
Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala		
245	250	255
Met Glu His Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu		
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Thr Asp Asn Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu		
275	280	285
Thr His Arg Val Ile Thr Arg Asn Lys		
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<211> 321

<212> PRT

<213> Arabidopsis sp.

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 20 25 30

20 Leu Met Ala Thr Ala Leu Asn Val Arg Val Pro Glu Ala Leu Ile Gly  
35 40 45

Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn  
 85 90 95

Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp Phe Leu Leu  
110

Val Val Met Cys Asn Ile 100 105 110  
 Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr Glu Val Val

Ser Arg Ala Cys Gly Ala Val 120 125  
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 Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly Glu Thr Met  
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130 135 140  
 Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp Tyr Tyr Met

Giá trị TAN =

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180	185		190
Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp			
195	200	205	
Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu			
210	215	220	
Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met			
225	230	235	240
Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp			
245	250	255	
Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly			
260	265	270	
Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala			
275	280	285	
Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp Val Lys Arg			
290	295	300	
Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile Thr Arg Asn			
305	310	315	320

Lys

<210> 13  
<211> 621  
<212> DNA  
<213> Arabidopsis sp.

<400> 13

gcttttcctt ttgctaattc tttagctttc ttgatccac cgcgatttct aactatttca	60
atcgcttcctt caagcgatcc aggctcacaa aactcagact caatgatctc tcttagcctt	120
ggctcattctt ctagcgcaa gatcactggc gccgttatgt tacctttggc taagtcatta	180
gctgcaggct tacctaactg ctctgtggac tgagtgaagt ccagaatgtc atcaactact	240
tgaaaagata aaccgagatt cttcccgAACAC tgatacatttt gctctgcgac cttgctttcg	300
actttactga aaattgtc tcctttggtg ctgcageta ctaatgaagc tgtcttgtag	360
taactcttta gcatgtagtc atcaagctt acatcacaaat cgaataaact cgatgcttgc	420
tttatctcac cgcttgaaaa atcttgcattt acctgcaaaa agataaatca agattcagac	480
caaatgttct ttgttattgag tagcttcatc taatctcaga aaggaatattt acctgactt	540
taagcttaat gacttcaagg ttttcgagat ttgtaaatgc catgtatgc ttgcaacatg	600
aaatccccag ctaatacagc t	621

<210> 14  
<211> 741  
<212> DNA  
<213> Arabidopsis sp.

<400> 14

ggtgagttt	gttaatagtt	atgagattca	tctatTTT	tcataaaatt	gtttggTTT	60
gtttaaactc	tgtgtataat	tgcaggaaag	gaaacagtcc	atgagCTTT	cggcacaaga	120
gttagCGGTGc	tagCTGGAGA	tttcatGTT	gctcaAGCGT	catggTactt	agcaaATCTC	180
gagaatCTTG	aagtattaa	gctcatAGT	caggtactta	gttactCTTA	cattGTTTT	240
ctatgaggTT	gagctatgaa	tctcatTTG	ttgaaaataatG	ctgtGCCtCA	aactTTTT	300
catgtttca	ggtgatcaa	gacttGCAA	gcggagagat	aaagcaggcg	tccagCTTat	360
ttgactgCGA	cacaagCTC	gacgaggACT	tactcaAAAG	tttctacaAG	acagCCTCTT	420
tagtgCTGc	gaggcacAAA	ggagCTGCA	tttCAGCAG	agttgaggCT	gatgtgacAG	480
aacaatGTA	cgagtTTGGG	aagaatCTG	gtctCTCTT	ccagatAGT	gatgatATT	540
tggattcac	tcagTCGACA	gaggCAGCTG	ggaaggCCAGC	agggagtGAT	ttggctAAAG	600
gtaacttaAC	agcacCTGT	atTTCTGCTC	tggagggGGA	gccaaggCTA	agagagatCA	660
ttgagtcAA	gttCTGTGAG	gcgggTTCTC	tggaaaAGC	gattgaaAGC	gtgacAAAG	720
gtggggggat	taagagAGCA	C				741

<210> 15  
<211> 1087  
<212> DNA  
<213> Arabidopsis sp.

<400> 15

cctcttcAGC	caatccAGAG	gaagaAGAGA	caactTTTA	tcttcGTC	agagtCTCCG	60
aaaACGcAcG	gttttatGCT	ctctttCTG	ccctCACCTC	acaAGACG	gggcACATGA	120
ttcaaccAGA	gggaaaaAGC	aacgataACA	actCTGCTT	tgatttCAAG	ctgtATATGA	180
tccgcaAAcG	cgagtCTGTA	aatgcggCTC	tcgacGTTT	cgtaccGCTT	ctgAAACCCC	240
ttacgatCCA	agaAGCGGT	aggtactTT	tgctAGCCG	cggAAAACGT	gtgaggCCtC	300
tgctCTGcat	tgccGTTGt	gagTTGTTG	ggggcGacGA	ggctactGCC	atgtcAGCCG	360
cttgcGCGGT	cgagatGATC	cacacaAGCT	ctctcATTCA	tgacgatTT	ccgtGCATGG	420
acaatGCCG	cctccGTA	ggcaAGCCCA	ccaatCACAA	gtatGTTGt	ttattatATA	480
gaaggGCTAG	agataatGCT	gaactAGTGT	tgaaccaATT	tttGCTCAA	caaggTATA	540
ggagaAGACA	tggcGGTTT	ggcaggGTAT	gcactCCTT	cattGCGCTT	tgacCACATG	600
acggTTGT	cgagtGGGTT	ggtcGCTCCC	gagaAGATGA	ttcGCGCCGT	gttGAGCTG	660
gccaggGCCA	tagggACTAC	aggGCTAGT	gctggacAAA	tgatAGACCT	agccAGCGAA	720
agactGAATC	cagacaAGGT	tggattGGAG	catCTAGAT	tcatCCATCT	ccacAAAACG	780
gcggcATTG	tggaggcAGC	ggcagTTTA	ggggTTATAA	tggaggTGG	aacAGAGGAA	840
gaaatCGAA	agcttagAAA	gtatGCTAGG	tgtattGGAC	tactGTTCA	gttGTTGAT	900
gacattCTCG	acgtaACAAA	atctactGAG	gaattGGGA	agacAGCCG	aaaAGACGTA	960
atggCCGGA	agctGAGCTA	tccaAGGCTG	ataggTTTG	agggatCCAG	ggaAGTTGCA	1020
gaggacCTGA	ggagAGAGC	agaggAAAAG	cttAAAGGGT	ttgatCCAAG	tcaggcGGCG	1080
cctctTGG						1087

<210> 16  
<211> 1164  
<212> DNA  
<213> Arabidopsis sp.

<400> 16

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cgaGTCGGAG	tcctCTCTCT	tcgGAATTG	gattCCGTTG	agttcaCTG	ccggCGTTCT	120
ggttTCTCGA	cgttgatcta	cgaatCACCC	gggcGGAGAT	ttgttGTCG	tgcggcGGAG	180
actgataCTG	ataaaAGTTAA	atctcAGACA	cctgacaAGG	caccAGCCG	tggTTCAAGC	240
attaaccAGC	tttCTGTTAT	caaaggAGCA	tctcaAGAAA	ctaataAAATG	gaagATTCTG	300
cttcAGCTTA	caaaaACCGT	cactTGGCCT	ccactGGTT	ggggAGTCGT	ctgtGGGTGCT	360
gctgCTTCAG	ggaACTTCA	ttggACCCCA	gaggatGTTG	ctaAGTCGAT	tctttGATG	420
atgatGTCG	gtcCTTGTCT	tactGGCTAT	acacAGACAA	tcaACGACTG	gtatGATAGA	480
gatatCAGC	caattaATGA	gcCATATCGT	ccaattCCAT	ctggAGCAAT	atcaGAGCCA	540
gaggTTATTA	cacaAGTCTG	ggtgCTATTA	ttgggAGGTC	ttggTATTG	tggAAATATTA	600

gatgtgtggg	cagggcatac	caactccact	gtcttctatc	ttgcctttggg	aggatcattg	660
ctatcttata	tatactctgc	tccacccctt	aagctaaaac	aaaatggatg	ggttggaaat	720
tttgcaactg	gagcaagcta	tattagtttgc	ccatgggtggg	ctggccaagc	attgtttggc	780
actcttacgc	cagatgttg	tgttctaca	ctctgtaca	gcatacgctgg	gttaggaata	840
gccatgtta	acgacttcaa	aagtgtgaa	ggagatagag	cattaggact	tcagtcctc	900
ccagtagctt	ttggcaccga	aactgcaaaa	tggatatgcg	ttggtgctat	agacattact	960
cagcttctg	ttggccggata	tctattagca	tctgggaaac	cttattatgc	gttggcggtg	1020
gttgcgttga	tcattcctca	gattgttttc	cagtttaaat	actttctcaa	ggaccctgtc	1080
aaatacgacg	tcaagtacca	ggcaagcgcg	cagccattct	tggtgctcg	aatatttgt	1140
acggcattag	catcgcaaca	ctga				1164

<210> 17

<211> 387

<212> PRT

<213> Arabidopsis sp.

<400> 17

Met	Thr	Ser	Ile	Leu	Asn	Thr	Val	Ser	Thr	Ile	His	Ser	Ser	Arg	Val
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															10

Thr	Ser	Val	Asp	Arg	Val	Gly	Val	Leu	Ser	Leu	Arg	Asn	Ser	Asp	Ser
															30
															25

Val	Glu	Phe	Thr	Arg	Arg	Arg	Ser	Gly	Phe	Ser	Thr	Leu	Ile	Tyr	Glu
															45
															35

Ser	Pro	Gly	Arg	Arg	Phe	Val	Val	Arg	Ala	Ala	Glu	Thr	Asp	Thr	Asp
															50
															55

Lys	Val	Lys	Ser	Gln	Thr	Pro	Asp	Lys	Ala	Pro	Ala	Gly	Gly	Ser	Ser
															60
															70

65	Ile	Asn	Gln	Leu	Leu	Gly	Ile	Lys	Gly	Ala	Ser	Gln	Glu	Thr	Asn	Lys
															95	
															85	

Trp	Lys	Ile	Arg	Leu	Gln	Leu	Thr	Lys	Pro	Val	Thr	Trp	Pro	Pro	Leu
															100
															105

Val	Trp	Gly	Val	Val	Cys	Gly	Ala	Ala	Ala	Ser	Gly	Asn	Phe	His	Trp
															115
															120

125	Thr	Pro	Glu	Asp	Val	Ala	Lys	Ser	Ile	Leu	Cys	Met	Met	Met	Ser	Gly
															130	
															135	

140	Pro	Cys	Leu	Thr	Gly	Tyr	Thr	Gln	Thr	Ile	Asn	Asp	Trp	Tyr	Asp	Arg
															145	
															150	

145	Asp	Ile	Asp	Ala	Ile	Asn	Glu	Pro	Tyr	Arg	Pro	Ile	Pro	Ser	Gly	Ala
															160	
															165	

165	Ile	Ser	Glu	Pro	Glu	Val	Ile	Thr	Gln	Val	Trp	Val	Leu	Leu	Leu	Gly
															180	
															185	

185	Gly	Leu	Gly	Ile	Ala	Gly	Ile	Leu	Asp	Val	Trp	Ala	Gly	His	Thr	Thr
															195	
															200	

200	Pro	Thr	Val	Phe	Tyr	Leu	Ala	Leu	Gly	Gly	Ser	Leu	Leu	Ser	Tyr	Ile
															210	
															215	

220

Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn  
 225 230 235 240  
 Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln  
 245 250 255  
 Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu  
 260 265 270  
 Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser  
 275 280 285  
 Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe  
 290 295 300  
 Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr  
 305 310 315 320  
 Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr  
 325 330 335  
 Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe  
 340 345 350  
 Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala  
 355 360 365  
 Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala  
 370 375 380  
 Ser Gln His  
 385

<210> 18  
 <211> 981  
 <212> DNA  
 <213> Arabidopsis sp.

<400> 18

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cacactcttc	ctatgaact	ctctcccgct	gcaatccgat	cttcatacctc	atctgccccg	120
gggtcggtga	acttcgatct	gaggacgtat	tggacgactc	tgatcacccga	gatcaaccag	180
aagctggatg	aggccatacc	ggtaaaggcac	cctgcggggga	tctacgaggc	tatgagatac	240
tctgtactcg	cacaaggcgc	caagcgtgcc	cctcctgtga	tgtgtgtggc	ggcctgccc	300
ctttcggtg	gcatcgcc	cggcccttcc	cccacccgcct	gtgccttaga	aatggcgcac	360
gcgcgttctgt	tgatacacga	cgacccccc	tgtatggacg	acgatcctgt	gcccggaggaa	420
aaggccatcta	accacactgt	ctacggctct	ggcatggcca	ttctcgccgg	tgacgcccc	480
ttcccactcg	ccttccagca	cattgtctcc	cacacgcctc	ctgacccctgt	tccccggagcc	540
accatccatca	gactcatcac	ttagattgcc	cgcactgtcg	gctccactgg	tatggctgca	600
ggccagtacg	tcgaccttga	aggagggtccc	tttcctttt	ccttgttca	ggagaagaaa	660
ttcggagcca	tgggtgaatg	ctctgcccgt	tgccgtggcc	tattggccgg	tgccactgag	720
gatgagctcc	agagtctcc	aaggtacggg	agagccgtcg	ggatgctgt	tcaggtggtc	780
gatgacatca	ccgaggacaa	gaagaagagc	tatgtatgtg	gagcagagaa	ggaaatgtatg	840
gaaatggccg	aagagctcaa	ggagaaggcg	aagaaggagc	ttcaagtgtt	tgacaacaag	900
tatggaggag	gagacacact	tgttcccttc	tacacccctcg	ttgactacgc	tgctcatcg	960
cattttcttc	ttccccctctg	a				981

<210> 19

<211> 245  
 <212> DNA  
 <213> Glycine sp.

<400> 19

gcaacatctg ggactgggtt	tgtcttgggg agtggtagtg	ctgttgcatt ttcggcactt	60
tcttcactt gcttgggtac	catgatggtt gctgcattctg	ctaactctt gaatcagggtg	120
tttggatca ataatgatgc	taaaatgaag agaacaagtgc	gcaggccact accctcagga	180
cgccatcacaa tacctcatgc	agttggctgg gcattccttg	ttggattagc tggtacggct	240
ctact			245

<210> 20  
 <211> 253  
 <212> DNA  
 <213> Glycine sp.

<400> 20

attggcttcc caagatcatt	gggtttctt gttgcattca	tgaccttcta ctcccttgggt	60
ttggcattgt ccaaggatat	acctgacgtt	gaaggagata aagagcacgg	120
tttgcagttac gtcttaggtca	gaaacgggca	ttttggattt gcttttcctt	180
gcttcggag ttggatcct	ggccggagca	tcatgctcac acttttggac	240
acgggtatgg gaa			253

<210> 21  
 <211> 275  
 <212> DNA  
 <213> Glycine sp.

<400> 21

tgatcttcta ctctctgggt	atggcattgt	ccaaggatat atctgacgtt	60
aaggatatacg	atcgataact	aaaggagata ttgttggattt	120
gcattatcct	ttttgaaatg	ttttggag ttgccttgc	180
accttggat	aaaattgtc	ggcaggagca acatcttctt	240
accaagccaa	atctatatac	tcttgcattca attctcttgt	275

<210> 22  
 <211> 299  
 <212> DNA  
 <213> Glycine sp.

<220>  
 <221> misc\_feature  
 <222> (1)...(299)  
 <223> n = A,T,C or G

<400> 22

ccanaatang tncatcttng	aaagacaatt ggccttca	acacacaagt ctgcattgtg	60
agaagaggcc aattgtctt	ccaagatcac ttatngtgc	tattgtaatc atgaacttct	120
tcttgggg tatggcattg	gcaaggata tacctanctg	ttgaaggaga taaaatatat	180
ggcattgata ctttgcatt	acgtataggc caaaaacaag	tattttggat ttgtattttc	240
cattttgaaa ggcttcgga	gtttccctag tggcaggagc	aacatcttct agccttgg	299

<210> 23  
 <211> 767

<212> DNA

<213> Glycine sp.

<400> 23

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tctgatgttg aaatagacaa gataaacaag ccgttatcttc cattagcata tgggaatat 120  
tccttgaaa ctgggtgtcac tattgttgca tcttttcaa ttctgagttt ttggcttggc 180  
tgggtttag gtcatggcc attattttgg gcctttttg taagctttgt gctaggaact 240  
gcttattcaa tcaatgtgccc tctgttgaga tggaaagaggt ttgcagtgtc tgcaagcgatg 300  
tgcatcttag ctgttcgggc agtaatagtt caacttgcat ttttccttca catcagact 360  
catgtgtaca agaggccacc tgtctttca agaccattga ttttgctac tgcatctatg 420  
agcttcttct ctgttagttt agcactttt aaggatatac ctgacattga aggagataaa 480  
gtatttggca tccaatctttt ttcagttgtt ttaggtcaga agccgggtgtt ctggacttgt 540  
gttacccttc ttgaaatagc ttatggagtc gccttcctgg tggagctgc atctcccttgt 600  
ctttggagca aaattttcac gggctggga cacgctgtgc tggcttcaat tctctggttt 660  
catgc当地 ctgttagattt gaaaagcaaa gttcgataa catcctcta tatgtttatt 720  
tggaaagctat ttatgcaga atacttactc attcctttt ttagatg 767

<210> 24

<211> 255

<212> PRT

<213> Glycine sp.

<400> 24

Val Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly  
1 5 10 15  
Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr  
20 25 30  
Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile  
35 40 45  
Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly  
50 55 60  
Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr  
65 70 75 80  
Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val  
85 90 95  
Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu  
100 105 110  
Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val  
115 120 125  
Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser  
130 135 140  
Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys  
145 150 155 160  
Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val  
165 170 175  
Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu

180	185	190
Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly		
195	200	205
Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser		
210	215	220
Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile		
225	230	235
Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg		
245	250	255

<210> 25  
<211> 360  
<212> DNA  
<213> Zea sp.

<220>  
<221> misc\_feature  
<222> (1)...(360)  
<223> n = A,T,C or G

<400> 25

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tcaggcttat cttggcctga cattcaactg gggagcttta ctagggggg ctgcattaa	120
ggaaggata gaccctgcaa atcatccttc cattgtatac agctgttatt tggtggacgc	180
tggtgtatga tactatatat ggcgcattagg ttgttcgcta tccctacttt catattaatc	240
cttgatgaag tggccatttc atgttgcgc ggtggctta tacttgcata tctccatgca	300
tctcaggaca aagangatga cctgaaaatgaa ggagtccaaag tccacagttt aagatttggg	360

<210> 26  
<211> 299  
<212> DNA  
<213> Zea sp.

<220>  
<221> misc\_feature  
<222> (1)...(299)  
<223> n = A,T,C or G

<400> 26

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aatggaaaagg acaatgcgtg cccctgccta tctggtcgca tttagtcctgc acatgctgc	120
atgtgggcta caagtgttgg agttgcagga acagctttgt tggctggaa ggctaatggc	180
ttggcagctg ggcttgccgc ttctaatctt gttctgtatg catttgcata tacgccgttg	240
aagcaatac accctgttaa tacatgggtt gggcagtcg ttggccat cccaccact	299

<210> 27  
<211> 255  
<212> DNA  
<213> Zea sp.

<220>  
<221> misc\_feature  
<222> (1)...(255)

<223> n = A, T, C or G

<400> 27

anacttgcat atctccatgc ntctcaggac aaagangatg acctgaaagt aggtgtcaag	60
tccacagcat taagatttg agatttgacc nnatactgna tcagtggctt tggcgccgca	120
tgcttcggca gcttagcact cagtggttac aatgctgacc ttggtttgtt tttagtgtga	180
tgcttggcg aagaatggta tngttttac ttgatattga ctccagacct gaaatcatgt	240
tggacagggt ggccc	255

<210> 28

<211> 257

<212> DNA

<213> Zea sp.

<400> 28

attgaagggg ataggactct ggggcttcag tcacttcctg ttgctttgg gatggaaact	60
gaaaaatgga ttgtgttgg agcaattgtt attcaat tatctgttg agttaccta	120
ttgagcaccc gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcagggt	180
ttcttcagt tccagttactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggca	240
agcgacacaac cattctt	257

<210> 29

<211> 368

<212> DNA

<213> Zea sp.

<400> 29

atccagttgc aaataataat ggcgttcttc tctgttgtaa tagcactatt caaggatata	60
cctgacatcg aaggggaccc catattcggg atccgatcct tcagcgtccg gttagggcaa	120
aagaaggctt tttggatctg cgttggcttg cttgagatgg cctacagcg tgcgatactg	180
atgggagcta cctcttcctg tttgtggagc aaaacagcaa ccattcgctgg ccattccata	240
cttggcgcga tcctatggag ctgcgcgcga tcgggtggact tgacgagcaa agccgcaata	300
acgtccttcat acatgttcat ctggaaagctg ttctacgcgg agtacctgct catccctctg	360
gtgcgggtg	368

<210> 30

<211> 122

<212> PRT

<213> Zea sp.

<400> 30

Ile Gln Leu Gln Ile Ile Met Ala Phe Phe Ser Val Val Ile Ala Leu	
1	5
10	15

Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg	
20	25
30	

Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val	
35	40
45	

Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr	
50	55
60	

Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile	

65	70	75	80
			Ser Val Asp Leu Thr Ser
Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg			
	85	90	95
Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr			
	100	105	110
Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg			
	115	120	

<210> 31  
<211> 278  
<212> DNA  
<213> Zea sp.

<400> 31

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gcgagttaca tcagcttgcc ctgggtggct ggccaggcgt tatttggAAC tcttacacca	120
gatatatcattg ttttgactac tttgtacacg atagctggc tagggattgc tattgtaaat	180
gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tggtgctttt	240
ggqatqgaaa ctgaaaaatg gatttgtgtt ggagcaat	278

<210> 32  
<211> 292  
<212> PRT  
<213> *Synechocystis* sp.

<400> 32

Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile  
20 25 30

Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu  
35 40 45

Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu  
50 55 60

Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val  
 65 70 75 80

Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln  
 85 90 95

Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu

100 105 110  
Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val

Ala Pro Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro  
 115 120 125  
 Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro  
 120 135 140

130 131  
Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp

145	150	155	160
Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly			
	165	170	175
Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala			
	180	185	190
Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe			
	195	200	205
Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr			
	210	215	220
Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu			
	225	230	240
Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr			
	245	250	255
Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile			
	260	265	270
Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu			
	275	280	285
Leu Gly Trp Leu			
	290		

<210> 33  
 <211> 316  
 <212> PRT  
 <213> Synechocystis sp.

<400> 33			
Met Val Thr Ser Thr Lys Ile His Arg Gln His Asp Ser Met Gly Ala			
	1	5	10
Val Cys Lys Ser Tyr Tyr Gln Leu Thr Lys Pro Arg Ile Ile Pro Leu			
	20	25	30
Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg			
	35	40	45
Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala			
	50	55	60
Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp			
	65	70	75
Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val			
	85	90	95
Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser			
	100	105	110
Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala			
	115	120	125

Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys  
 130 135 140  
 Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile  
 145 150 155 160  
 Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr  
 165 170 175  
 Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe  
 180 185 190  
 Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val  
 195 200 205  
 Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile  
 210 215 220  
 Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr  
 225 230 235 240  
 Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu  
 245 250 255  
 Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly  
 260 265 270  
 Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu  
 275 280 285  
 Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His  
 290 295 300  
 Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly  
 305 310 315

<210> 34  
 <211> 324  
 <212> PRT  
 <213> Synechocystis sp.

<400> 34  
 Met Ser Asp Thr Gln Asn Thr Gly Gln Asn Gln Ala Lys Ala Arg Gln  
 1 5 10 15  
 Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys  
 20 25 30  
 Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp  
 35 40 45  
 Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val  
 50 55 60  
 Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu  
 65 70 75 80  
 Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile  
 85 90 95

Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser  
 100 105 110  
 Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile  
 115 120 125  
 Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile  
 130 135 140  
 Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser  
 145 150 155 160  
 Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala  
 165 170 175  
 Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu  
 180 185 190  
 Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser  
 195 200 205  
 Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu  
 210 215 220  
 Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile  
 225 230 235 240  
 Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala  
 245 250 255  
 Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr  
 260 265 270  
 Ile Val Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr  
 275 280 285  
 Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala  
 290 295 300  
 Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly  
 305 310 315 320  
 His Ala Gly Ile

<210> 35  
 <211> 307  
 <212> PRT  
 <213> Synechocystis sp.

<400> 35

Met Thr Glu Ser Ser Pro Leu Ala Pro Ser Thr Ala Pro Ala Thr Arg	15
1 5 10	
Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val	30
20 25	
Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln	45
35 40	

Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile  
 50 55 60  
 Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly  
 65 70 75 80  
 Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg  
 85 90 95  
 Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu  
 100 105 110  
 Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu  
 115 120 125  
 Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro  
 130 135 140  
 Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr  
 145 150 155 160  
 Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser  
 165 170 175  
 Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr  
 180 185 190  
 Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu  
 195 200  
 Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly  
 210 215 220  
 Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala  
 225 230 235 240  
 Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile  
 245 250 255  
 Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr  
 260 265 270  
 His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn  
 275 280 285  
 Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala  
 290 295 300  
 Gly Leu Gly  
 305

<210> 36  
 <211> 927  
 <212> DNA  
 <213> Synechocystis sp.

<400> 36  
 atggcaacta tccaagcttt ttggcgcttc tcccgcccccc ataccatcat tggtacaact 60

ctgagcgtct	gggctgtgta	tctgttaact	attctcgaaa	atggaaactc	agtaaactcc	120
cctgcgttccc	tggatttagt	gttcggcgct	tggctggcct	gcctgttggg	taatgtgtac	180
attgtcggcc	tcaaccattt	gtgggatgtg	gacattgacc	gcatcaataa	gccgaatttg	240
ccccatgtca	acggagattt	ttctatcgcc	cagggccgtt	ggattgtggg	actttgtggc	300
gttgcgttcc	tggcgtatcg	ctggggattt	ggctatggc	tggggctaac	gggtgggcatt	360
agttttagtt	ttggcacggc	ctattcggt	ccgcccagtga	ggttaaagcg	ctttccctg	420
ctggccggcc	tgtgtattct	gacgggtcg	ggaattgtgg	ttaacttggg	cttattttta	480
tttttagaa	ttgggtttag	ttatcccccc	actttaataa	cccccatctg	ggttttgact	540
ttatttatct	tagtttcac	cgtggcgtac	gcattttta	aagatgtgcc	agatatggaa	600
ggcgatcgcc	aatttaagat	tcaaactta	actttgcaaa	tcggcaaaaca	aaacgtttt	660
cggggAACCT	taattttact	cactgggtt	tathtagcca	tggcaatctg	gggcttatgg	720
gcggctatgc	ctttaataac	tgctttctt	attgttccc	attgtgtctt	attagccta	780
ctctgtggc	ggagtcgaga	tgtacactta	gaaagcaaaa	ccgaaattgc	tagttttat	840
cagtttattt	ggaagctattt	tttcttagag	tacttgctgt	atcccttggc	tctgtggta	900
cctaattttt	ctaatactat	tttttag				927

<210> 37

<211> 308

<212> PRT

<213> Synechocystis sp.

<400> 37

Met	Ala	Thr	Ile	Gln	Ala	Phe	Trp	Arg	Phe	Ser	Arg	Pro	His	Thr	Ile
1				5					10					15	

Ile	Gly	Thr	Thr	Leu	Ser	Val	Trp	Ala	Val	Tyr	Leu	Leu	Thr	Ile	Leu
							25						30		

Gly	Asp	Gly	Asn	Ser	Val	Asn	Ser	Pro	Ala	Ser	Leu	Asp	Leu	Val	Phe
							40					45			

Gly	Ala	Trp	Leu	Ala	Cys	Leu	Leu	Gly	Asn	Val	Tyr	Ile	Val	Gly	Leu
						55					60				

Asn	Gln	Leu	Trp	Asp	Val	Asp	Ile	Asp	Arg	Ile	Asn	Lys	Pro	Asn	Leu
65					70				75				80		

Pro	Leu	Ala	Asn	Gly	Asp	Phe	Ser	Ile	Ala	Gln	Gly	Arg	Trp	Ile	Val
								85				90		95	

Gly	Leu	Cys	Gly	Val	Ala	Ser	Leu	Ala	Ile	Ala	Trp	Gly	Leu	Gly	Leu
							100					105		110	

Trp	Leu	Gly	Leu	Thr	Val	Gly	Ile	Ser	Leu	Ile	Ile	Gly	Thr	Ala	Tyr
							115					120		125	

Ser	Val	Pro	Pro	Val	Arg	Leu	Lys	Arg	Phe	Ser	Leu	Leu	Ala	Ala	Leu
						130		135				140			

Cys	Ile	Leu	Thr	Val	Arg	Gly	Ile	Val	Val	Asn	Leu	Gly	Leu	Phe	Leu
							145		150			155		160	

Phe	Phe	Arg	Ile	Gly	Leu	Gly	Tyr	Pro	Pro	Thr	Leu	Ile	Thr	Pro	Ile
							165		170			175			

Trp	Val	Leu	Thr	Leu	Phe	Ile	Leu	Val	Phe	Thr	Val	Ala	Ile	Ala	Ile
							180		185			190			

Phe	Lys	Asp	Val	Pro	Asp	Met	Glu	Gly	Asp	Arg	Gln	Phe	Lys	Ile	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195	200	205
Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu		
	210	215
Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp		
	225	230
Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys		
	245	250
Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser		
	260	265
Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe		
	275	280
Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser		
	290	295
Asn Thr Ile Phe		
	305	

<210> 38  
 <211> 1092  
 <212> DNA  
 <213> Synechocystis sp.

<400> 38

atgaaatttc cgccccacag tggtaaccat tggcaaggct aatcaccttt ctttgaaggt	60
tggtaacgtgc gcctgctttt gccccaatcc ggggaaagtt ttgcttttat gtactccatc	120
gaaaatctgt cttagcgatca tcattacggc ggccgtgtct tgcaaatttt agggccggct	180
acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa	240
aaattttggg ccagtccctcg ccaggttgcc cttagggcatt ggggaaaatg tagggataac	300
aggcaggcga aaccctact ctccgaagaa tttttgcga cggtaagga aggttatcaa	360
atccatcaaa atcagcacca aggacaaatc attcatggcg atccgcatttgc tcgttggca	420
ttcaccgttag aaccggaagt aactggggg agtcctaacc gatttctcg ggctacagcg	480
ggttggcttt cctttttacc cttgtttgat cccggttggc aaattttttt agcccaaggt	540
agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgcacca cggccctagtt	600
tatgccgaaa aaaattgggg tcactccctt ccctcccgct gttttggct ccaagcaaat	660
tatttccctg accatccagg actgagcgctc actgccgtg gcggggaaacg gattgttctt	720
ggtcgccccg aagaggtagc tttaattggc ttacatcacc aaggttaattt ttacgaattt	780
ggcccggggcc atggcacagt cacttggcaa gtagctccctt gggggccgtt gcaattaaaa	840
gccaagcaatg ataggatttgc ggtcaagttt tccggaaaaa cagataaaaaa aggcaatttt	900
gtccacactc ccaccgcccc gggcttacaa ctcaactgcc gagataccac tagggcttat	960
ttgtatattgc aattgggatc tgtgggtcac ggcctgatag tgcaaggggaa acggacacc	1020
gcggggcttag aagttggagg tgattgggt ttaacagagg aaaattttag caaaaaaaaca	1080
gtgccattct ga	1092

<210> 39  
 <211> 363  
 <212> PRT  
 <213> Synechocystis sp.

<400> 39

Met Lys Phe Pro Pro His Ser Gly Tyr His Trp Gln Gly Gln Ser Pro	
5	10
	15

Phe Phe Glu Gly Trp Tyr Val Arg Leu Leu Leu Pro Gln Ser Gly Glu  
20 25 30

Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His  
35 40 45

Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln  
50 55 60

Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys  
65 70 75 80

Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys  
85 90 95

Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe  
100 105 110

Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly  
115 120 125

Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu  
130 135 140

Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala  
145 150 155 160

Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu  
165 170 175

Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln  
180 185 190

Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His  
195 200 205

Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp  
210 215 220

His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu  
225 230 235 240

Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn  
245 250 255

Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala  
260 265 270

Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val  
275 280 285

Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro  
290 295 300

Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr  
305 310 315 320

Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly  
325 330 335

Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr  
340 345 350

Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe  
355 360

<210> 40  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide adapter

<400> 40 56  
cgcgatttaa atggcgcgcc ctgcaggcgg ccgcctgcag ggcgcgccat ttaaat

<210> 41  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 41 32  
tcgaggatcc gcggccgcaa gtttcttgca gg

<210> 42  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 42 32  
tcgacctgca ggaagcttgc ggccgcggat cc

<210> 43  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 43 32  
tcgacctgca ggaagcttgc ggccgcggat cc

<210> 44  
<211> 32

<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 44

tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 45  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 45

tcgaggatcc gcggccgcaa gcttcctgca ggagct 36

<210> 46  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 46

cctgcaggaa gcttgcgccc gcggatcc 28

<210> 47  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 47

tcgacctgca ggaagcttgc ggccgcggat ccagct 36

<210> 48  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 48

ggatccgcgg cccgaagctt cctgcagg 28

<210> 49  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 49  
gatcacctgc aggaagcttg cggccgcgga tccaatgca 39

<210> 50  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 50  
ttggatccgc ggccgcaagg ttcctgcagg t 31

<210> 51  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 51  
ggatccgcgg ccgcacaatg gagtctctgc tctcttagttc t 41

<210> 52  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 52  
ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

<210> 53  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 53  
ggatccgcgg ccgcacaatg gcgtttttg ggctctcccg tttt 45

<210> 54  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 54  
ggatcctgca gtttattgaa aacttcttcc aagtacaact 40

<210> 55  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 55  
ggatccgcgg ccgcacaatg tggcgaagat ctgttg 38

<210> 56  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 56  
ggatcctgca ggtcatggag agtagaagga aggagct 37

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotides

<400> 57  
ggatccgcgg ccgcacaatg gtacttgccg aggttccaaa gcttgctct 50

<210> 58  
<211> 38  
<212> DNA

<213> Artificial Sequence  
<220>  
<223> Synthetic Oligonucleotides  
<400> 58 38  
ggatcctgca ggtcacttgt ttctggtgat gactctat

<210> 59  
<211> 38  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic Oligonucleotides  
<400> 59 38  
ggatccgcgg ccgcacaatg acttcgattc tcaacact

<210> 60  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic Oligonucleotides  
<400> 60 36  
ggatcctgca ggtcagtgtt gcgatgctaa tgccgt

<210> 61  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Region of slr1736 open reading frame  
<400> 61 22  
taatgtgtac attgtcgccc tc

<210> 62  
<211> 60  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Region of slr1736 open reading frame  
<400> 62 60  
gcaatgttaac atcagagatt ttgagacaca acgtggctt ccacaattcc ccgcaccgtc

<210> 63  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Region of slr1736 open reading frame

<400> 63 22

aggctaataa gcacaaatgg ga

<210> 64  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Region of slr1736 open reading frame

<400> 64 60  
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggaattgg ttttagttat 63  
ccc

<210> 65  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 65 26

ggatccatgg ttgcccaaac cccatc

<210> 66  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 66 60  
gcaatgtaac atcagagatt ttgagacaca acgtggctt gggtaagcaa caatgaccgg 61  
c

<210> 67  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Oligonucleotide primer  
<400> 67  
gaattctcaa agccagccca gtaac 25

<210> 68  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer  
<400> 68  
ggtatgagtc agcaacacct tcttcacgag gcagacacta gcgggtgcga aaagggtttt 60  
ccc 63

<210> 69  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> End of open reading frame fragment  
<400> 69  
ccagtgggtt aggctgtgtg gtc 23

<210> 70  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> End of open reading frame fragment  
<400> 70  
ctgagttgga tgtattggat c 21

<210> 71  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer  
<400> 71  
ggatccatgg ttacttcgac aaaaatcc 28

<210> 72

<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 72

gcaatgtAAC atcAGAGATT ttGAGACACA acGTGGCTT GCTAGGCAAC CGCTTAGTAC 60

<210> 73  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 73

gaattcttaa cccAACAGTA aAGTTCCC 28

<210> 74  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer

<400> 74

ggTATGAGTC AGCAACACCT TCTTCACGAG GCAGACCTCA GCGCCGGCAT TGTCTTTAC 60  
atg 63

<210> 75  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Open reading frame fragment

<400> 75

ggaacccttg cagccgcTTc 20

<210> 76  
<211> 22  
<212> DNA  
<213> Artificial Sequence

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<400> 94

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 <213> Glycine sp.

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<211> 1188

<212> DNA

<213> Glycine sp.

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<211> 395

<212> PRT

<213> Glycine sp.

<400> 97

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Arg Lys Ile Gln Lys Glu Tyr Asn Phe Leu Arg Phe Arg Trp Pro Ser  
35 40 45

Leu Asn His His Tyr Lys Ser Ile Glu Gly Gly Cys Thr Cys Lys Lys  
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Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Phe Glu  
65 70 75 80

Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys  
85 90 95

Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile  
100 105 110

Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys  
115 120 125

Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val  
130 135 140

Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu  
145 150 155 160

Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr Leu Pro Leu Ala  
165 170 175

Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe  
180 185 190

Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly Ser Trp Pro Leu  
195 200 205

Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr Ala Tyr Ser Ile  
210 215 220

Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met  
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Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu  
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His Ile Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Ser  
260 265 270

Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala  
275 280 285

Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Val Phe Gly Ile  
290 295 300

Gln Ser Phe Ser Val Arg Leu Gly Gln Lys Pro Val Phe Trp Thr Cys  
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Val Ile Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu Leu Val Gly Ala

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Asn Ile Tyr His Ala Ser Ser Tyr Val Pro Asn Ala Ser Trp His Asn		
35	40	45
Arg Lys Ile Gln Lys Glu Tyr Asn Phe Leu Arg Phe Arg Trp Pro Ser		
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Leu Asn His His Tyr Lys Gly Ile Glu Gly Ala Cys Thr Cys Lys Lys		
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Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Leu Glu		
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Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys		
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Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile		
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Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys		
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Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val		
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Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe		
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 Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met  
 245 250 255  
 Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu  
 260 265 270  
 His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Pro  
 275 280 285  
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 290 295 300  
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 305 310 315 320  
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 325 330 335  
 Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu Leu Val Gly Ala  
 340 345 350  
 Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly Leu Gly His Ala  
 355 360 365  
 Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser Val Asp Leu Lys  
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 <212> DNA  
 <213> Oryza sp.

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<210> 101  
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<213> Allium porrum

<400> 101

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<212> DNA  
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<400> 102

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<212> DNA  
<213> Zea sp.

<400> 106

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ccctccactc cacttgcata ctcgtcggt cgtcgccgc cgttccccc cggcccaagg 180  
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gcatatttgc agttcgatgc gtttgcgttgc agctggcctt ttttgcgttgc attcagactt 600  
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<210> 107  
<211> 362  
<212> DNA  
<213> *Gossypium* sp.

<400> 107

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tgcattttctt	ggttccggac	ttctactgggt	gaattatgtt	gctgctgtgt	tggctgcaat	180
atacatgcct	caggcttca	ggcgtagttt	aatgataacct	gctcatatatct	ttttggcggt	240
ctgcttgatt	tttcagacat	gggtgttggaa	acaagcaaat	tacaaaaagg	aagcaatctc	300
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gt						362

<210> 108

<211> 575

<212> DNA

<213> Lycopersicon sp.

<400> 108

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aatagacaag	gttacacaagc	catatcttcc	atggcatca	gggaaatact	ctgtacaaac	540
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<210> 109

<211> 1663

<212> DNA

<213> *Arabidopsis* sp.

<400> 109

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ccatttcgtat	ggAACACCTC	ggaagtctt	cgagggatgg	tggatccggg	tttccatccc	360
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tcttggcgct	aatgataaat	atttatgcca	atacgaacaa	gactctcaca	attctgggg	540
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aaacaaggag	gttccaccag	aggaatttaa	cagaagagt	tccgaagggt	tccaagctac	660
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gaaatctgct	cgttgggagt	atagactcg	tcccgttac	ggttgggtg	atgttggggc	780
caaacagaag	tcaactgcag	gctggctgc	agctttcct	gtatggagc	ctcattggca	840
gatatgcgt	gcaggaggcc	tttccacagg	gtggatagaa	tggggcggtg	aaaggttga	900
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<210> 110  
<211> 488  
<212> PRT  
<213> Arabidopsis sp.

<400> 110

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Phe Arg Ser Thr Lys Leu Val Pro Arg Ser Ile Ser Arg Val Ser Ala  
35 40 45  
Ser Ile Ser Thr Pro Asn Ser Glu Thr Asp Lys Ile Ser Val Lys Pro  
50 55 60  
Val Tyr Val Pro Thr Ser Pro Asn Arg Glu Leu Arg Thr Pro His Ser  
65 70 75 80  
Gly Tyr His Phe Asp Gly Thr Pro Arg Lys Phe Phe Glu Gly Trp Tyr  
85 90 95  
Phe Arg Val Ser Ile Pro Glu Lys Arg Glu Ser Phe Cys Phe Met Tyr  
100 105 110  
Ser Val Glu Asn Pro Ala Phe Arg Gln Ser Leu Ser Pro Leu Glu Val  
115 120 125  
Ala Leu Tyr Gly Pro Arg Phe Thr Gly Val Gly Ala Gln Ile Leu Gly  
130 135 140  
Ala Asn Asp Lys Tyr Leu Cys Gln Tyr Glu Gln Asp Ser His Asn Phe  
145 150 155 160  
Trp Gly Asp Arg His Glu Leu Val Leu Gly Asn Thr Phe Ser Ala Val  
165 170 175  
Pro Gly Ala Lys Ala Pro Asn Lys Glu Val Pro Pro Glu Glu Phe Asn  
180 185 190  
Arg Arg Val Ser Glu Gly Phe Gln Ala Thr Pro Phe Trp His Gln Gly  
195 200 205  
His Ile Cys Asp Asp Gly Arg Thr Asp Tyr Ala Glu Thr Val Lys Ser  
210 215 220  
Ala Arg Trp Glu Tyr Ser Thr Arg Pro Val Tyr Gly Trp Gly Asp Val  
225 230 235 240

Gly Ala Lys Gln Lys Ser Thr Ala Gly Trp Pro Ala Ala Phe Pro Val  
 245 250 255  
 Phe Glu Pro His Trp Gln Ile Cys Met Ala Gly Gly Leu Ser Thr Gly  
 260 265 270  
 Trp Ile Glu Trp Gly Gly Glu Arg Phe Glu Phe Arg Asp Ala Pro Ser  
 275 280 285  
 Tyr Ser Glu Lys Asn Trp Gly Gly Phe Pro Arg Lys Trp Phe Trp  
 290 295 300  
 Val Gln Cys Asn Val Phe Glu Gly Ala Thr Gly Glu Val Ala Leu Thr  
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 Ala Gly Gly Leu Arg Gln Leu Pro Gly Leu Thr Glu Thr Tyr Glu  
 325 330 335  
 Asn Ala Ala Leu Val Cys Val His Tyr Asp Gly Lys Met Tyr Glu Phe  
 340 345 350  
 Val Pro Trp Asn Gly Val Val Arg Trp Glu Met Ser Pro Trp Gly Tyr  
 355 360 365  
 Trp Tyr Ile Thr Ala Glu Asn Glu Asn His Val Val Glu Leu Glu Ala  
 370 375 380  
 Arg Thr Asn Glu Ala Gly Thr Pro Leu Arg Ala Pro Thr Thr Glu Val  
 385 390 395 400  
 Gly Leu Ala Thr Ala Cys Arg Asp Ser Cys Tyr Gly Glu Leu Lys Leu  
 405 410 415  
 Gln Ile Trp Glu Arg Leu Tyr Asp Gly Ser Lys Gly Lys Val Ile Leu  
 420 425 430  
 Glu Thr Lys Ser Ser Met Ala Ala Val Glu Ile Gly Gly Pro Trp  
 435 440 445  
 Phe Gly Thr Trp Lys Gly Asp Thr Ser Asn Thr Pro Glu Leu Leu Lys  
 450 455 460  
 Gln Ala Leu Gln Val Pro Leu Asp Leu Glu Ser Ala Leu Gly Leu Val  
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 Pro Phe Phe Lys Pro Pro Gly Leu  
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<210> 111  
 <211> 246  
 <212> PRT  
 <213> Arabidopsis sp.

<400> 111  
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35	40	45
Leu Asp Ile Gln Gly Lys Phe Val Ile Phe Thr Val Ile Gly Val Tyr		
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Leu Glu Gly Asn Ala Val Pro Ser Leu Ser Val Lys Trp Lys Gly Lys		
65	70	80
Thr Thr Glu Glu Leu Thr Glu Ser Ile Pro Phe Phe Arg Glu Ile Val		
85	90	95
Thr Gly Ala Phe Glu Lys Phe Ile Lys Val Thr Met Lys Leu Pro Leu		
100	105	110
Thr Gly Gln Gln Tyr Ser Glu Lys Val Thr Glu Asn Cys Val Ala Ile		
115	120	125
Trp Lys Gln Leu Gly Leu Tyr Thr Asp Cys Glu Ala Lys Ala Val Glu		
130	135	140
Lys Phe Leu Glu Ile Phe Lys Glu Glu Thr Phe Pro Pro Gly Ser Ser		
145	150	155
Ile Leu Phe Ala Leu Ser Pro Thr Gly Ser Leu Thr Val Ala Phe Ser		
165	170	175
Lys Asp Asp Ser Ile Pro Glu Thr Gly Ile Ala Val Ile Glu Asn Lys		
180	185	190
Leu Leu Ala Glu Ala Val Leu Glu Ser Ile Ile Gly Lys Asn Gly Val		
195	200	205
Ser Pro Gly Thr Arg Leu Ser Val Ala Glu Arg Leu Ser Gln Leu Met		
210	215	220
Met Lys Asn Lys Asp Glu Lys Glu Val Ser Asp His Ser Leu Glu Glu		
225	230	235
Lys Leu Ala Lys Glu Asn		
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<210> 112  
 <211> 3115  
 <212> DNA  
 <213> Arabidopsis sp.

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aatgcttca gtatgtttt agtattacaa agttgtaaaga ttttattttt attcatttg 540  
tggctcacca ttgcacgact actttgaat tttagttttt gaaaaatgca attaacatc 600  
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tattatgtat gtatgattt agttcggtcg gtcctgtgg taaatgatac gggccagtgt 3060  
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<210> 113  
<211> 536  
<212> DNA  
<213> Arabidopsis sp.

<400> 113

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ctgtatctcc tctcaacttcg tcacttagttc cggtccgatc gactaaacta gttccccgt 180  
ccatcttag ggtttcggcg tcgatctcca ccccgaaatag tgaaactgac aagatctccg 240  
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cagagaagag ggagagttt tggttatgt attctgtgaa gaatcctgca ttccggcaga 420  
gtttgttacc atttggaaatgt gctctatatg gaccttagatt cactgggtt ggagctcaga 480  
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<210> 114  
<211> 411  
<212> PRT  
<213> Arabidopsis sp.

<220>  
<223> Peptide PIR: T04448 shown in Figure 31

<400> 114

Pro Glu Lys Arg Glu Ser Phe Cys Phe Met Tyr Ser Val Glu Asn Pro  
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Arg Phe Thr Gly Val Gly Ala Gln Ile Leu Gly Ala Asn Asp Lys Tyr  
35 40 45

Leu Cys Gln Tyr Glu Gln Asp Ser His Asn Phe Trp Gly Asp Arg His  
50 55 60

Glu Leu Val Leu Gly Asn Thr Phe Ser Ala Val Pro Gly Ala Lys Ala  
65 70 75 80

Pro Asn Lys Glu Val Pro Pro Glu Glu Phe Asn Arg Arg Val Ser Glu  
85 90 95

Gly Phe Gln Ala Thr Pro Phe Trp His Gln Gly His Ile Cys Asp Asp  
100 105 110

Gly Arg Thr Asp Tyr Ala Glu Thr Val Lys Ser Ala Arg Trp Glu Tyr  
115 120 125

Ser Thr Arg Pro Val Tyr Gly Trp Gly Asp Val Gly Ala Lys Gln Lys  
130 135 140

Ser Thr Ala Gly Trp Pro Ala Ala Phe Pro Val Phe Glu Pro His Trp  
145 150 155 160

Gln Ile Cys Met Ala Gly Gly Leu Ser Thr Gly Trp Ile Glu Trp Gly  
165 170 175

Gly Glu Arg Phe Glu Phe Arg Asp Ala Pro Ser Tyr Ser Glu Lys Asn  
180 185 190

Trp Gly Gly Phe Pro Arg Lys Trp Phe Trp Val Gln Cys Asn Val  
195 200 205

Phe Glu Gly Ala Thr Gly Glu Val Ala Leu Thr Ala Gly Gly Gly Leu  
210 215 220

Arg Gln Leu Pro Gly Leu Thr Glu Thr Tyr Glu Asn Ala Ala Leu Val  
225 230 235 240

Cys Val His Tyr Asp Gly Lys Met Tyr Glu Phe Val Pro Trp Asn Gly  
245 250 255

Val Val Arg Trp Glu Met Ser Pro Trp Gly Tyr Trp Tyr Ile Thr Ala  
260 265 270

Glu Asn Glu Asn His Val Val Glu Leu Glu Ala Arg Thr Asn Glu Ala  
275 280 285

Gly Thr Pro Leu Arg Ala Pro Thr Thr Glu Val Gly Leu Ala Thr Ala  
290 295 300

Cys Arg Asp Ser Cys Tyr Gly Glu Leu Lys Leu Gln Ile Trp Glu Arg  
305 310 315 320

Leu Tyr Asp Gly Ser Lys Gly Lys Leu Lys Val Leu Thr Asn Pro Lys  
325 330 335  
Ala Val Lys Glu Asp Tyr Glu Arg Leu Leu Trp Leu Thr Met Met Gln  
340 345 350  
Val Ile Leu Glu Thr Lys Ser Ser Met Ala Ala Val Glu Ile Gly Gly  
355 360 365  
Gly Pro Trp Phe Gly Thr Trp Lys Gly Asp Thr Ser Asn Thr Pro Glu  
370 375 380  
Leu Leu Lys Gln Ala Leu Gln Val Pro Leu Asp Leu Glu Ser Ala Leu  
385 390 395 400  
Gly Leu Val Pro Phe Phe Lys Pro Pro Gly Leu  
405 410